

re-nm

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Application Serial Number: 10/828,564
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DATE: 03/07/2005

PATENT APPLICATION: US/10/828,564

TIME: 16:23:49

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1 <110> APPLICANT: PALESE, PETER
2     BASLER, CHRISTOPHER F.
3     GARCIA-SASTRE, ADOLFO
4 <120> TITLE OF INVENTION: CHRIS-LIKE VIRUS, COMPOSITIONS, VACCINES AND USES THEREOF
5 <130> FILE REFERENCE: PP-26000-US
6 <140> CURRENT APPLICATION NUMBER: US/10/828,564
7 <141> CURRENT FILING DATE: 2004-04-21
8 <150> PRIOR APPLICATION NUMBER: 60/483,337
9 <151> PRIOR FILING DATE: 2003-06-27
10 <160> NUMBER OF SEQ ID NOS: 18
11 <170> SOFTWARE: PatentIn Ver. 3.2
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1690
15 <212> TYPE: DNA
16 <213> ORGANISM: Homo sapiens
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Output Set: N:\CRF4\03072005\J828564.raw

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56      20          25          30
57      Thr Tyr Gly Arg Ser Ala Ile Gln Glu Pro Ser Thr Arg Ala Arg Ile
58      35          40          45
59      Gln Ser Trp Glu Ser Arg Asn Pro Asp His Asp Tyr Thr Gly Asn Lys
60      50          55          60
61      Asn Gln Arg Ser Glu Gly Ala Lys Glu Arg Ala Asn Lys Ser Glu Ser
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68      115         120         125
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70      130         135         140
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74      165         170         175
75      Ala Glu Thr Leu Gly Ser Ser Thr Gln Leu Thr Thr Met Arg Asn Ala
76      180         185         190
77      Thr Thr Asp Asp Phe Ala Lys Ile Phe Glu Glu Gly Thr Pro Lys Val
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79      His Arg Arg Leu Arg Gly Ile Thr Ala Val Val Pro Ala Gln Lys Gln
80      210         215         220
81      Pro Gly Ala Val Gly Gly Pro Val Lys Lys Gly Thr Asp Gly Ser Thr
82      225         230         235         240
83      Ala Ser Thr Leu Leu Gly Asp Val Pro Leu Ser Gly Ser Gly Ala Ile
84      245         250         255
85      Pro Asn Val His Pro Ser Leu Leu His Gln Pro Lys Lys Asn Ala His
86      260         265         270
87      Ala Glu Asn Ala Gln Gly Ser Val Gln Asp Val Ser Thr Thr Gly Ala
88      275         280         285
89      Ile Gly Gln Ser Asp Glu Ala Ala His Phe Asp Gln Glu Ile Glu Gly
90      290         295         300
91      Lys Leu Asn Leu Val Leu Lys Glu Leu Asp Leu Ile Ser Lys Lys Leu
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93      Asp Tyr Leu Pro Glu Ile Lys Glu Glu Ile Arg Asn Ile Asn Lys Lys
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99 <211> LENGTH: 1690
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101 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 3
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105      agcttggtcaa ggatggaatc aagactatcg agctttttaca gcagagtccg gaagactttc 180
106      agaagacgta cggcagaagt gccatccagg agccgtcgac aagagccaga atccaaagtt 240
107      gggagtcctcg caatcccgat catgattaca ccggtataaa aaatcagaga agcgagggag 300
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134 <211> LENGTH: 347
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 4
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140      Ile Lys Thr Ile Glu Leu Leu Gln Gln Ser Pro Glu Asp Phe Gln Lys
141      20          25          30
142      Thr Tyr Gly Arg Ser Ala Ile Gln Glu Pro Ser Thr Arg Ala Arg Ile
143      35          40          45
144      Gln Ser Trp Glu Ser Arg Asn Pro Asp His Asp Tyr Thr Gly Asn Lys
145      50          55          60

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147       65                               70                               75                               80
148   Ala Gly Thr Ala Ser Ala Asp Gly Gly His Gly Asp Lys Pro Ser Asn
149                               85                               90                               95
150   Asn Gly Gly Asp Ser Gln Asn Glu Tyr Gln Gly Ser Asp Gln Gln Val
151                               100                              105                              110
152   Trp Asp Ala Ala Tyr Asn Asp Gly Asn Ser Gly Gly Ala Trp Gly Gly
153                               115                              120                              125
154   Pro Thr Gly Gly Leu Pro Thr Ala Gly Glu Arg Gly Tyr Pro Ile Thr
155                               130                              135                              140
156   Thr Gly Asn Gln Glu Phe Glu Gly Tyr His Pro Asp Gly Pro Val Asp
157   145                               150                               155                               160
158   Ala Arg Glu Tyr Asn Gln Ile Ser Ser Met Asp His Glu Met Ser Ala
159                               165                               170                               175
160   Ala Glu Thr Leu Gly Ser Ser Thr Gln Leu Thr Thr Met Arg Asn Ala
161                               180                              185                              190
162   Thr Thr Asp Asp Phe Ala Lys Ile Phe Glu Glu Gly Thr Pro Lys Val
163                               195                              200                              205
164   His Arg Arg Leu Arg Gly Ile Thr Ala Val Val Pro Ala Gln Lys Gln
165                               210                              215                              220
166   Pro Gly Ala Val Gly Gly Pro Val Lys Lys Gly Thr Asp Gly Ser Thr
167   225                               230                               235                               240
168   Ala Ser Thr Leu Leu Gly Asp Val Pro Leu Ser Gly Ser Gly Ala Ile
169                               245                               250                               255
170   Pro Asn Val His Pro Ser Leu Leu His Gln Pro Lys Lys Asn Ala His
171                               260                              265                              270
172   Ala Glu Asn Ala Gln Gly Ser Val Gln Asp Val Ser Thr Thr Gly Ala
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174   Ile Gly Gln Ser Asp Glu Ala Ala His Phe Asp Gln Glu Ile Glu Gly
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178   Asp Tyr Leu Pro Glu Ile Lys Glu Glu Ile Arg Asn Ile Asn Lys Lys
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180   Ile Thr Asn Leu Ser Leu Gly Leu Leu Tyr Ser
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183 <210> SEQ ID NO: 5

184 <211> LENGTH: 2493

185 <212> TYPE: DNA

186 <213> ORGANISM: Homo sapiens

187 <400> SEQUENCE: 5

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190   tgcagtgggt ggcctaagtc ttcattgtctg tatcaagggg aagatgagca atgcccttaa 180
191   ggctcagcta ggatacaaaa ccacgatttg ttattctctc atggacacca acccgtaact 240
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231 <210> SEQ ID NO: 6

232 <211> LENGTH: 242

233 <212> TYPE: PRT

234 <213> ORGANISM: Homo sapiens

235 <400> SEQUENCE: 6

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239          20             25             30
240      Ile Pro Gly Arg Ser Tyr Asp Leu Lys Thr Ser Thr Gln Ala Ser Tyr
241          35             40             45
242      Gln Tyr Met Val Ile Lys Leu Ile Pro Asn Val Asn Gly Leu Asn Asn
243          50             55             60
244      Cys Thr Asn Ser Thr Val Glu Ser Tyr Lys Lys Met Leu Thr Arg Leu
245          65             70             75             80

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VERIFICATION SUMMARY

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